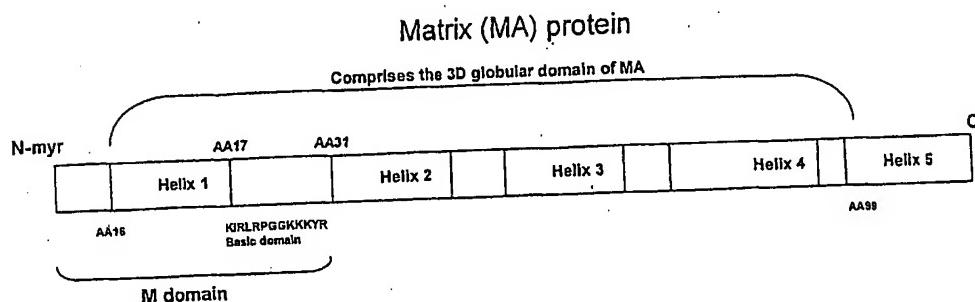
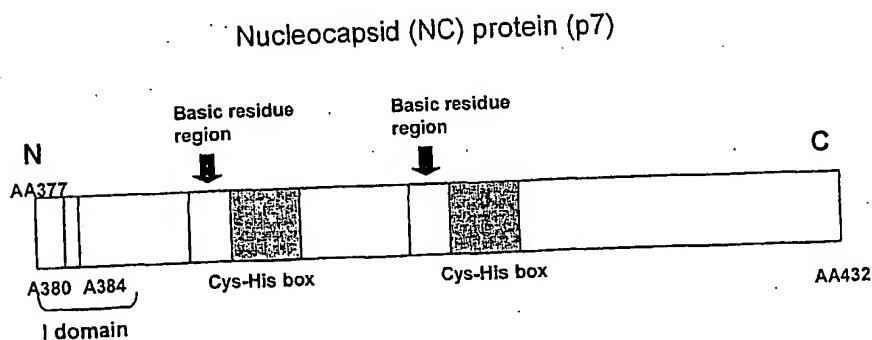
**Figure 1****Figure 2****Figure 3**

2/6

Capsid (CA) protein (p24)

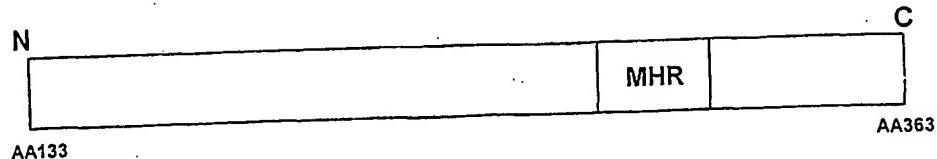


Figure 4

P6 protein

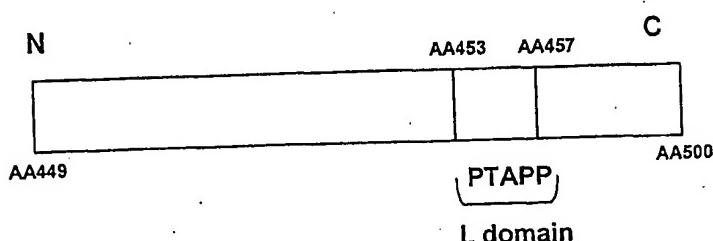


Figure 5

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1   GAATTTCATGG GTGCGAGAGC GTCAATATTA AGAGGGAAA ATTAGATAA ATGGGAAAAAG
61  ATTAGGTAA GCCCAGGGG AAAGAAACAT TATATGTTAA AACACATAGT ATGGCGAGC
121 AGGGAGCTGG AAAGATTGCT ACTTAACCCCT GGCTTTTG AAACATCAGA AGGATGAAA
181 CAAATAATGA AACAGCTACA ACCAGCTCTC CAGACAGGAA CAGAGGAAC TAAATCATTAA
241 TACAAACACAG TAGCAACTCT CTATTGTGTA CATGAAAAGA TAGAAGTAGC AGACACCAAG
301 GAAGCCTTAG ATAAGATAGA GGAAGAACAA AACAAATGTC AGCAAAAC GCAGCAGGCA
361 AAAGCGGTG ACAGGAAAGT CAGTCAAAAT TATCCTATAAG TCAGAAATCT CCAAGGGCAA
421 ATGGTACATC AAGCCATATC ACCTAGAACCC TTGAATGCAT GGGTAAARGT AATAGAAGAA
481 AAGCTTTTA GCCCAGAGGT AATACCCATG TTTCAGCAGT TATCAGAAGG AGCCACCCCCA
541 CAAGATTTAA ACACCATGT AAATACAGTG GGGGGACACC AAGCAGCCAT GCAAATGTTA
601 AAAGATACTA TTAAATGAAGA GGCTGCAGAA TGGGATAGAT TACATCCAGT CCATGGGGGG
661 CCTATTGCA CAGGCCAGAT GAGAGAACCA AGGGGAAGTG ACATAGCAGG AACTACTAGT
721 ACCCTTCAGG AACAATATGC ATGGATGACA AGTAACCCAC CTATTCCACT GGGAGACATC
781 TATAAAAGAT GGATAATTCT GGGGTTAAAT AAAATAGTGA GAATGTATAG CCCGGTCAGC
841 ATTTTGAGC TAAGACAAAGG GCCAAAGGAA CCCTTTCAGG ACTATGTAGA TCGGTCTTT
901 AAAACTTTAA GAGCTGAACA AGCTACACAA GAAGTAAAAA ATTGGATGAC AGACACCTTG
961 TTAGTCAAA ATGCCAACCC AGATTGTAAG ACCATTGTA GAGCATAGG ACCAGGGCT
1021 ACATTAGAAG AAATGATGAC AGCATGTCAA GGGGTGGGG GACCTGGCCA CAAAGCAAGA
1081 GTATTGGCTG AGGCAATGAG TCAAAACAAAC AGTGGAAACA TAATGATGCA GAGAAGCAAT
1141 TTTRAAAGGC CTAGAAGAAT TGTTAAATGT TTAAACTGTG GCAAGGAAGG GCACATAGCC
1201 AGAAATTGCA GAGCCCCTAG GAAAAAAAGGC TGTGGAAT GTGGAAAAGA AGGACACCAA
1261 ATGAAAGACT GCACTGAGAG GCAGGCTAAAT TTTTTAGGGA AAATTGGCC TTCCCCACAG
1321 GGGAGGCCAG GGAATTTCCT TCAGAACAGA CCAGAGCCAA CAGCCCCCACC AGCAGAGAGC
1381 TTCAGGGTCG AAGAGAACAC CCCCGCTCCG AAAAGAGAGC CGATAGAAGG GGAACCCCTTA
1441 ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGTCTC AATAAAAGTA GGGGGCCAGA
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Figure 6

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3/6

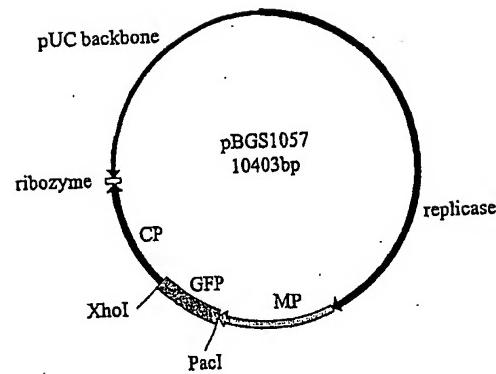


Figure 7

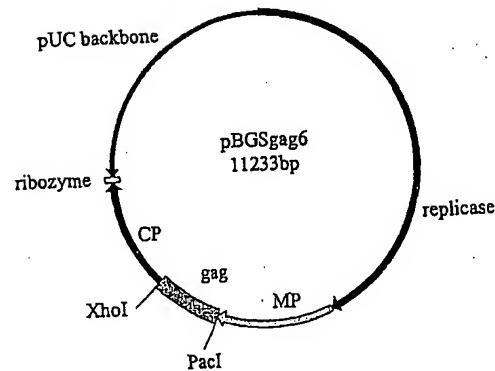


Figure 8

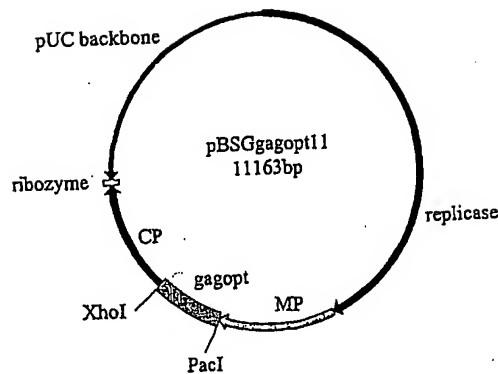


Figure 9

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 61 TTAAGGCCAG GGGGAAAGAA ACATTATATG TTAAAACACA TAGTATGGGC GAGCAGGGAG
 121 CTGGAAAGAT TTGCACTTAA CCCTGGCCCTT TTAGAACAT CAGAAGGATG TAAACAAATA
 181 ATGAAACAGC TACAACCAGC TCTCCAGACA GGAACAGAGG AACTTAAATC ATTATACAAAC
 241 ACAGTAGCAA CTCTCTATTG TGTACATGAA AAGATAGAAG TAGCAGACAC CAAGGAAGCC
 301 TTAGATAAGA TAGAGGAAGA ACAAAACAAA TGTCAGCAA AAACGCAGCA GGCAAAAGCG
 361 GCTGACGGGA AAGTCAGTC AAATTATCCT ATAGTGCAAGA ATCTCCAAGG GCAAATGGTA
 421 CATCAAGCCA TATCACCTAG AACCTTGAAT GCATGGGTAA AGTAATAGA AGAAAAGGCT
 481 TTTAGGCCAG AGGTAAATAC CATGTTTACA GCATTATCAG AGGGAGCCAC CCCACAAGAT
 541 TTAAACACCA TGTTAAATAC AGTGGGGGGA CACCAAGCAG CGATGCAAAT GTTAAAAGAT
 601 ACTATTAAATG AAGAGGTGTC AGAATGGGT AGATTACATC CAGTCCATGC GGGGCCTATT
 661 GCACCAGGGC AGATGAGAGA ACCAAGGGGA AGTGCACATAG CAGGAACATAC TAGTACCCCT
 721 CAGGAACAAA TAGCATGGAT GACAAGTAAC CCACCTATTG CAGTGGGAGA CATCTATAAA
 781 AGATGGATAA TTCTGGGGTT AAATAAAATA GTGAGAATGT ATAGCCCCTG CAGCATTGG
 841 GACATAAGAC AAGGGCCAAA GGAACCCCTT CGAGACTATG TAGATCGGTT CTTTAAACT
 901 TTAAGAGCTG AACAAAGCTAC ACAAGAGTA AAAAATTGGGA TGACAGACAC CTTGTTAGTC
 961 CAAAATGCGA ACCCAGATTG TAAGACATT TTGAGAGCAT TAGGACCAGG GGCTACATTA
 1021 GAAGAAAATGA TGACAGCATG TCAAGGGCTG GGAGGACCTG GCCACAAAGC AAGAGTATTG
 1081 GCTGAGGCAA TGAGTCAAAC AAACAGTGGG AACATAATGA TGAGAGAAG CAATTTAAA
 1141 GGCCTAGAA GAATTGTTAA ATGTTTTAAC TGTTGGCAAGG AAGGGCACAT AGCCAGAAAT
 1201 TGCGAGGCC CTAGGAAAAA AGGCTGTTGG AAATGTGGAA AAGAAGGACA CCAAATGAAA
 1261 GACTGCAGTG AGAGGCAGGC TAATTTTTA GGGAAAATTG GGCTTCCCCA CAAGGGGAGG
 1321 CCAGGGAAATT TCCTTCAGAA CAGACCGAG CCAACAGCCC CACCGCAGA GAGCTTCAGG
 1381 TTGCAAGAGA CAACCCCCGC TCCGAAACAG GAGCCGATAG AAAGGGAAACC CTTAACTTCC
 1441 CTCAAATCAC TCTTGCGAG CGACCCCTTG TCTCAATAA

Figure 10

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WO 2004/050691

5/6

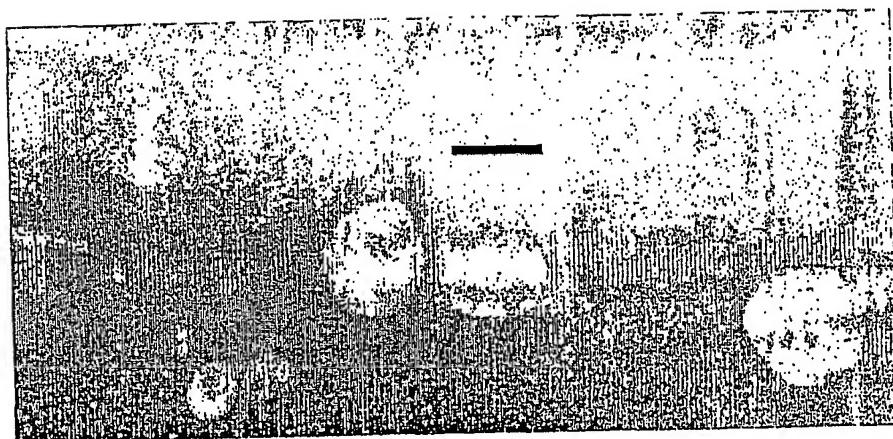


Figure 11

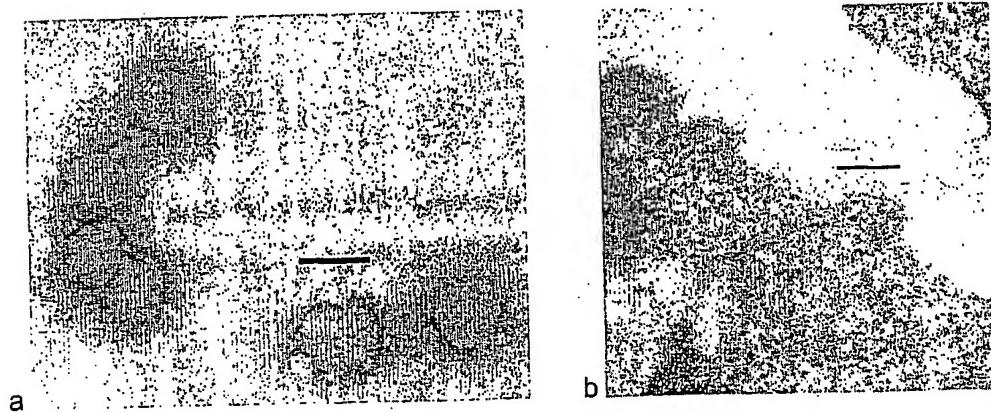


Figure 12

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6/6

EEFMGARASIL RGEKLDKWEK IRLRPGGKKH YMLKHIVWAS RELERFALNP GLLETSEGCK	60
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KAADGKVVSQN YPIVQNLQGQ MVHQAIISPRT LNAWKVIEE KAFSPREVPM FTALSEGATP	180
QDLNTMLNTV GGHQAAMQMI KDTINEEAAE WDRLHPVHAG PIAPGQMREP RGSDIAGTTS	240
TLQEIQIAWMN SNPPIPVGDI YKRWIILGLN KIVRMYSVPS ILDIRQGPKE PFRDYVDRFF	300
KTLRAEQATQ EVKNWMTDNL LVQNANPDCK TILRALGPGA TLEEMMTACQ GVGGPGHKAR	360
VLAEAMSQTN SGNIMMQRSN FKGPRIVKC FNGKEGHIA RNCRAPRKKG CWKCGKEGHQ	420
MKDCTERQAN FLGKIWPSHK GRPGNFIQNR PEPTAPPAES FFEETTPAP KQEPIEREPL	480
TSLKSLFGSD PLSQKGARQG RLSTQEQQM IQ YCR	513

Figure 13

MGARASILRG EKLDKWEKIR LRPGGKKHYM LKHIVWASRE LERFALNPGL LETSEGCKQI	60
MKQLQPALQT GTEELKSLYN TVATLYCVHE KIEVRDTKEA LDKIEEEQNK CQQKTQAKA	120
ADGKVVSQNYP IVQNLQGQMV HQAISPRTLN AWVKVIEEKA FSPEVIPMFT ALSEGATPOD	180
LNTMLNTVGG HQAAMQMIKD TINEEAAEWL RLHPVHAGPI APGQMREPRG SDIAGTTSTL	240
QEIQIAWMNSN PPIPVGDIYK RWIILGLNKI VRMYSVPSIL DIRQGPKEPF RDYVDRFFKT	300
LRAEQATQEV KNWMTDLLV QNANPDCKTI LRALGPGATL EEMMTACQGV GGGPGHKARVL	360
AEAMSQTNSG NIMMQRSNFK GPRRIVKCFN CGKEGHIA RNCRAPRKKG CWKCGKEHQMK	420
DCTERQANFL GKIWPSHKGR PGNFIQNRPE PTAPPAESFR FEETTPAPKQ EPIEREPLTS	480
LKSLFGSDPL SQ	

Figure 14